

THIS PAGE BLANK (USPTO)

RESULT 2

af056218
TOIG of: af056218 check: 414 from: 1 to: 1855

LOCUS AF056218 1855 bp mRNA linear MAM 05-MAR-1999
DEFINITION Bos taurus superficial zone protein mRNA, partial cds.
ACCESSION AF056218
VERSION AF056218.1 GI:3676500

KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
MAMMalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 1855)
Flannery,C.R., Hughes,C.E., Schumacher,B.L., Tudor,D.,
Aydelotte,M.B., Kuettner,K.E. and Caterson,B.
Articular cartilage superficial zone protein (SZP) is homologous to
megakaryocyte stimulating factor precursor and is a multifunctional
proteoglycan with potential growth-promoting, cytoprotective, and
lubricating properties in cartilage metabolism
Biochem. Biophys. Res. Commun. 254 (3), 535-541 (1999)

JOURNAL 99120896
MEDLINE 9920774
PUBMED 9920774

REFERENCE 2 (bases 1 to 1855)
Schumacher,B.L., Hughes,C.E., Kuettner,K.E., Caterson,B. and
Aydelotte,M.B.
Immunodetection and partial cDNA sequence of the proteoglycan,
superficial zone protein, synthesized by cells lining synovial
joints
J. Orthop. Res. 17 (1), 110-120 (1999)

JOURNAL 99171663
MEDLINE 10073655
PUBMED 10073655

REFERENCE 3 (bases 1 to 1855)
Schumacher,B.L.
Direct Submission
Submitted (31-MAR-1998) Biochemistry Jelle 1306, Rush University,
1653 W. Congress Pkwy., Chicago, IL 60612, USA
Location/Qualifiers

FEATURES
source
1..1855
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cell_type="chondrocyte"
/tissue_type="articular cartilage"
<1..1206
/codon_start=1
/product="superficial zone protein"
/protein_id="AADI3404.1"
/db_xref="GI:3676501"
/translation="EFPPVKGATNSQVTTKPKQKAPKPKTSKKPRTPVRKPK
TTPFPKTTSAMPEPTSLPEAMLQITRTPTPNSIIDVNSBEDGDAAGEKP
HMFPPVLTPIPTGTEIIVRGSGQGFNMFSDENLNCNRPVGLITLRNGILV
AFRGHYFPLTPPTPPPRITVEVGIPTDITFTRCNCEGKTFPKGSQYWRFTN
DKDAGYPKLISKGGNGKIVAAISIAQKSRPESVYFPRGSGVQYTYKQEPYQ
KCTGRPAISVYGETAQVRRRPERAIGPSOVHTIRIHYTPVRVYODKGFHNEV
KSTWRGLPNVVSISLPIRKPDGDYDVALSKDQYINIDVPSRTARAITTRSGQT
LSNTWYNCP"

BASE COUNT 638 a 418 c 312 g 487 t
ORIGIN

AF056218 Length: 1855 February 4, 2004 16:21 Type: N Check: 414
af056218

Alignment Scores:

Pred. No.: 0 Length: 1855
Score: 1713.50 Matches: 320
Percent Similarity: 86.22% Conservative: 24
Best Local Similarity: 80.20% Mismatches: 52
Query Match: 22.77% Indels: 3
Gaps: 1

US-09-556-246-1 (1-1404) x af056218 (1-1855)

QY 1007 ProLysAspArgAlaThrAsnSerLysAlaThrThrProLysProGlnLysProThrLys 1026
DB 13 CCAAAAGGCGAGAGTACTAATTTCTCAAGTGACAACCTCTTAACCGCAGAAACCAACAA 72
QY 1027 AlaProLysProThrSerThrLysLysLysMetProArgValArgLysPro 1046
DB 73 GCACCCCAAAAGGCCACTTCGACCAAAAGCCAAAGAACAA---CCTAGAGTGAGAAACCA 129
QY 1047 LysThrThrProThrProArgLys---MetThrSerThrMetProGluLeuAsnProThr 1065
DB 130 AGAGTAGGCCACGCCCCCAAGAGCAGCAGCATCAGCAATGCTGAAACCGACTCTTACC 189
QY 1066 SerArgLysAlaGluAlaMetLeuGlnThrThrArgProAsnGlnThrProAsnSer 1085
DB 190 TCT---TTACCAGAAGCCATGCTCCAAACCAACCCAGGCTTACCCCAACCCCACTCA 246
QY 1086 LysLeuValGluValAsnProLysSerGluAspAlaGlyGlyAlaGluGlyGluThrPro 1105
DB 247 GAAATAATTGCGTAAACTCAGAGATGAGATGGAGATGCTGCTGAAGGAGAAACCT 306
QY 1106 HisMetLeuLeuArgProHisValPheMetProGluValThrProAspMetAspTyrLeu 1125
DB 307 CACATGATTTTCAGCCCTGCTGCTAATCTTATAGTGATTCAGGCACTGAAATCATA 366
QY 1126 ProArgValProAsnGlnGlyIleIleAsnProMetLeuSerAspGluThrAsnIle 1145
DB 367 GTGAGAGGACCCAGCTCAAGGCTTCGGCATCAACCCCATGTTTTCAGATGAACATACTA 426
QY 1146 CysAsnGlyProValAspGlyLeuThrThrLeuArgAsnGlyThrLeuValAlaPhe 1165
DB 427 TGCACCGTAGGCGAGTAGATGGACTGACTTGTGCTAATGGGACATTAAGTTGCATTT 486
QY 1166 ArgGlyHisTyrPheTyrMetLeuSerProPheSerProPheSerProAlaArgArgIle 1185
DB 487 CGAGTCATATTTCTGGATCTGACTGCTGCTTACTCCACCACCTCCACCTCGGAGATT 546
QY 1186 ThrGluValTyrGlyIleProSerProIleAspThrValPheThrArgCysAsnGly 1205
DB 547 ACTGAAGTTTGGGCGATTTCCTCCCTCCCTGATGATGATGATGATGATGATGATGATG 606
QY 1206 GlyLysThrPhePheLysAspSerGlnTyrTyrPheThrAsnAspIleLysAsp 1225
DB 607 GGAAAAATCTTCTTTTAAAGGTTCTCAGTACTGCGCTTCCACCAATGATATATAAGAT 666
QY 1226 AlaGlyTyrProLysProIlePheLysGlyPheGlyLeuThrGlyGlnIleValAla 1245
DB 667 GCAGGATATCCCAACTAATTTCCAAAGGATTTGGAGGACTGAATGGAATAATAGTGCA 726
QY 1246 AlaLeuSerThrAlaLysTyrLysAsnTyrProGluSerValTyrPhePheLysArgGly 1265
DB 727 GCGCTCTCAATAGCTCAGTACAAAGAGCAGACCTGTAATCCGTGTATTTTTTCAAGAGGT 786
QY 1266 GlySerIleGlnGlnTyrIleTyrLysGlnGluProValGlnLysCysProGlyArgArg 1285
DB 787 GGCACGGTTTCAGCAATACACTTACAAACAGGAACCCACCCAAAGTGTACTGGAAGAGG 846
QY 1286 ProAlaLeuAsnTyrProValTyrGlyGluMetThrGlnValArgArgArgPheGlu 1305
DB 847 CTGCGATTAATATTTCTGTATGGAGAAACAGCAGCAGCTTAGGAGACGTCGATTTGAA 906
QY 1306 ArgAlaIleGlyProSerGlnThrHisThrIleArgIleGlnTyrSerProAlaArgLeu 1325
DB 907 CGTGCTATAGGACCTTCTCAAGTACACACCATCAGGATTCACCTACACACCCGTCAGAGTC 966
QY 1326 AlaTyrGlnAspLysGlyValLeuHisAsnGluValLysValSerIleLeuTyrAspGly 1345
DB 967 CCTTATCAAGACAAAGGTTTCTCCATAATGAATGAATGAATGAATGAATGAATGAAT 1026
QY 1346 LeuProAsnValValThrSerAlaIleSerLeuProAsnIleArgLysProAspGlyTyr 1365
DB 1027 CTTCCAAATGTGTTACTTTCAGCAGCATATCCTGCCCCCAACATCAGAAACCCGATGCTAT 1086

THIS PAGE BLANK (USPTO)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[illegible]

```

RESULT 2
af056218
; TOIG of: af056218 check: 414 from: 1 to: 1855
;
; LOCUS AF056218 1855 bp mRNA linear MAM 05-MAR-1999
; DEFINITION Bos taurus superficial zone protein mRNA, partial cds.
; ACCESSION AF056218
; VERSION AF056218.1 GI:3676500
; KEYWORDS
; SOURCE Bos taurus (cow)
; ORGANISM
; Bos taurus
; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
; Bovidae; Bovinae; Bos.
;
; REFERENCE
; 1 (bases 1 to 1855)
; Flannery,C.R., Hughes,C.E., Schumacher,B.L., Tudor,D.,
; Aydelotte,M.B., Kuettner,K.E. and Caterson,B.
; Articular cartilage superficial zone protein (SZP) is homologous to
; megakaryocyte stimulating factor precursor and is a multifunctional
; proteoglycan with potential growth-promoting, cytoprotective, and
; lubricating properties in cartilage metabolism
; Biochem. Biophys. Res. Commun. 254 (3), 535-541 (1999)
; 99120896
; MEDLINE
; PUBMED
; REFERENCE
; 2 (bases 1 to 1855)
; Schumacher,B.L., Hughes,C.E., Kuettner,K.E., Caterson,B. and
; Aydelotte,M.B.
; Immunodetection and partial cDNA sequence of the proteoglycan,
; superficial zone protein, synthesized by cells lining synovial
; joints
; J. Orthop. Res. 17 (1), 110-120 (1999)
; 99171663
; MEDLINE
; PUBMED
; REFERENCE
; 3 (bases 1 to 1855)
; Schumacher,B.L.
; Direct Submission
; Submitted (31-MAR-1998) Biochemistry Jelke 1306, Rush University,
; 1653 W. Congress Pkwy., Chicago, IL 60612, USA
;
; FEATURES
; source
; /organism="Bos taurus"
; /mol_type="mRNA"
; /db_xref="taxon:9913"
; /cell_type="chondrocyte"
; /tissue_type="articular cartilage"
; <1..1206
; /codon_start=1
; /product="superficial zone protein"
; /protein_id="AADI3404.1"
; /db_xref="GI:3676501"
; /translation="EPPVPKGRATNSQVTTPKQKPTKAPKPTSTKKPRTPRVRKPK
; TTPTPKTTISAMPEPTPTSLBEAMLTITRTPTPNSIIDVNSNEDGDAEGKEP
; HMFPRPVLMTPTPTPPRRITEVWGIPSPIDTFTRCNCEGKTFPFKGSQYWRFTN
; AFRGHVFMLTPTPTPPRRITEVWGIPSPIDTFTRCNCEGKTFPFKGSQYWRFTN
; DIKDAGYKPLISGFGKGLKIVAAISIAQYKSRPESVVFVKRGSVOQYTKQBPQ
; KCTGREPALNSVYGETAQRERRERERAIQPSQVHTIRLHVTVPVQDKGFLNEV
; KYSLWRGLPNVTSALSIPNIRKPKDGYALSKDQYINIDVPSRTARAITRSQT
; LSNTWNCBP"
;
; CDS
;
; BASE COUNT 638 a 418 c 312 g 487 t
; ORIGIN
;
; AF056218 Length: 1855 February 4, 2004 16:21 Type: N Check: 414 ..
; af056218
;
; Alignment Scores:
; Pred. No.: 0 Length: 1855
; Score: 1713.50 Matches: 320
; Percent Similarity: 86.22% Conservative: 24
; Best Local Similarity: 80.20% Mismatches: 52
; Query Match: 22.77% Indels: 3
; DB: 1 Gaps: 3

```

US-09-556-246-1 (1-1404) x af056218 (1-1855)

```

Qy 1007 ProLysAspArgAlaThrAsnSerLysAlaThrThrProLysProGlnLysProThrLys 1026
Db 13 CCAAAAGCGAGAGTACTAATTTCTCAAGTCACACTCTCTAAACCGCAGAAACCAACCAA 72
Qy 1027 AlaProLysLysProThrSerThrLysLysProLysThrMetProArgValArgLysPro 1046
Db 73 GCACCCAAAAGGCCACTTCGACCAAAAAGCAAGAACA--CCTAGAGTGAGAAAACCA 129
Qy 1047 LysThrThrProThrProArgLys--MetThrSerThrMetProGluLeuAsnProThr 1065
Db 130 AAGACTACGCCAACGCCCCCAAGACGACGACATCAGCAATGCTCGTGAACCGACTCTTACC 189
Qy 1066 SerArgIleAlaGluAlaMetLeuGlnThrThrArgProAsnGlnThrProAsnSer 1085
Db 190 TCT---TTACAGAAAGCCATGCTCCAAACCAACACAGGCTACCCCAACCCCACTCA 246
Qy 1086 LysLeuValGluValAsnProLysSerGluAspAlaGlyGlyAlaGluGlyGluThrPro 1105
Db 247 GAAATAATTGACGTAAACTCAGAGAAATGAGATGGAGATGCTGCTGAAGGAGAAAAACCT 306
Qy 1106 HisMetLeuLeuArgProHisValPheMetProGluValThrProAspMetAspTyrLeu 1125
Db 307 CACATGATTTTCAGGCCCTCTGCTAACTCTATAGTGATTCAGGCACCTGAAATCAT 366
Qy 1126 ProArgValProAsnGlnGlyIleIleAsnProMetLeuSerAspGluThrAsnIle 1145
Db 367 GTGAGAGCCAGCTCAAGGCTTCGGCATCAACCCCATGTTTCAGATGAATAACTACTA 426
Qy 1146 CysAsnGlyLysProValAspGlyLeuThrThrLeuArgAsnGlyThrLeuValAlaPhe 1165
Db 427 TGCAACGGTAGGCCAGTAGATGACTACTTTTGGTAATGGGACATTAGTTGCTATT 486
Qy 1166 ArgGlyHisTyrPheThrMetLeuSerProPheSerProProSerProAlaArgArgIle 1185
Db 487 CGAGGTCAATATTTCTGGATGCTGACTCCATTTTACCACCACTCCACCTCGGAGATT 546
Qy 1186 ThrGluValTyrGlyIleProSerProIleAspThrValPheThrArgCysAsnCysGlu 1205
Db 547 ACTGAAGTTTGGGCACTCTCCCTCCCATTTGATCTGTTTCTAGTATGCACTGTA 606
Qy 1206 GlyLysThrPhePheLysAspSerGlnTyrTrpArgPheThrAsnAspIleLysAsp 1225
Db 607 GGAATAACTTTCTTTAAGGGTCTCAGTACTGGCGTTTCCCAATATATATAAAGAT 666
Qy 1226 AlaGlyTyrProLysProIlePheLysGlyPheGlyLeuThrGlyGlnIleValAla 1245
Db 667 GCAGGATATCCAAACTAAATTTCCAAAGGATTTGGAGGACTGAATGGAATAATAGTGCA 726
Qy 1246 AlaLeuSerThrAlaLysTyrLysAsnTrpProGluSerValTyrPhePheLysArgGly 1265
Db 727 GCCCTCTCAATAGCTCAGTACAAGACGACCTGAATCCGTGTAATTTTTCAGAGAGGT 786
Qy 1266 GlySerIleGlnGlnTyrIleTyrLysGlnGluProValGlnLysCysProGlyArgArg 1285
Db 787 GGCAGCGTTCCAGCAATACACTTACAAACAGAAACCCCAACCAAGTGTACTGGAAGAAG 846
Qy 1286 ProAlaLeuAsnTyrProValTyrGlyLeuMetThrGlnValArgArgArgPheGlu 1305
Db 847 CCTGCGATAAACTATTCTGTGTATGGAGAAACACACAGAGGTAGGAGACGTCGATTGAA 906
Qy 1306 ArgAlaIleGlyProSerGlnThrHisThrIleArgIleGlnTyrSerProAlaArgLeu 1325
Db 907 CGTGTATAGACCTTCTCAAGTACACCATCAGGATTCCTACACCCCGTCAGAGTC 966
Qy 1326 AlaTyrGlnAspLysGlyValLeuHisAsnGluValLysValSerIleLeuTyrArgGly 1345
Db 967 CTTTATCAAGACAAAGGTTTCTCCATATAATGAAGTTAAAGTACACTACACTGTGAGAGA 1026
Qy 1346 LeuProAsnValValThrSerAlaIleSerLeuProAsnIleArgLysProAspGlyTyr 1365
Db 1027 CTTCCAAATGTGGTTACTTCAGCAATATCACTGCCCAACATCAGAAAAACCGATGGCTAT 1086

```



```
;
; BPAATTPKKPAPTTTKEBPAPTTPKPEPATTTTTTKKPAPTAKPEBAPTTPKETAPTTPKKK
; TPTTEKLAPITPPKBPAPTDEELAPTTPEEPTTTTBEPAPTTPPKAAPNTPKPEAPA
; TTPEBPAPTTPKBPAPTTPKTGTAATTTLKBPAFTTPKPBAPTELAPTTTKE
; PTSTTSOKPAPTTPKGTAATTPKBPAPTTPKGPAPTTPGTATPTLKBPAFTTPKKA
; PKELAPTTTGKPTSTSISDKPAPTTTKEATAATTPKBPAPTTPKGAATTPETPDPTTSE
; VSTTPKTKEPTTIHKSDESPTSLSAEPTPKALENSPKPEGVPTTKTPAATKPDMITT
; ADKTTTERDLATTBTETTAAIKMETATEITTEKTESKITATTQTOSTTTQDTPRK
; ITLUKTTTLABKVLTNMTTIIITEIMNKPEETAKEKRATNSKATTPKCKQPKKAPKAC
; PTVSKPKTMPVRPRKPTTPTRKMSTSMPELNPTSRABANMLQTTTRNRQTNPSKLIV
; EYNSKEDSAGAEGETPHMLLRPHVMEPVETPMDDYLPRVPNOGIIINMPLSDETNIC
; NGKVPDGLTLLRNGLTAVGHYPFWMLGPSFSPARRITVEANGIPSPIDTVFRNCN
; EGKTFPKDSOYWRFTNDIADQAGYFKPIPKFGGGLTGOJVAALSTAASKNWPSVYFF
; KRGSIOQYYIQBPOVKCGRRRPALNPVTVGEMTQVRERRPERAIGRSOTHTIRLOY
; DVARSLADKGVHLHNNEVSILMRGLPNVNITSALSLEPNIRKPDGDVDYYAFSKDOYINI
; SPSRLARAITRGSGDTLSKWYNCP"
; BASE COUNT      1710 a   1516 c    806 g   1009 t
; ORIGIN
; U0136 Length: 5041 February 4, 2004 16:21 Type: N Check: 6448 ..
; u0136
Alignment Scores:
Pred. No.:          0           Length:         5041
Score:             53.00        Matches:         17
Percent Similarity: 37.50%     Conservative:    4
Best Local Similarity: 30.36%  Mismatches:       21
Query Match:       0.70%      Indels:         14
DB:                1           Gaps:            2
US-09-556-246-1 (1-1404) x u0136 (1-5041)
Qy      28 SerSerCyseAlaGllyArgCyseGlyglugLyTyrserArgAepAlaThrCyseAnCysasp 47
Db      2832 AGCAGTTGTAGTTTCAGGTGTAGTAGCTACTCT----- 2797
Qy      48 TyrAsnCyseGlnHisTyMetGluCyCyseProasppheLysargValCyseThrAlaGlu 67
Db      2796 ---TTCCTGTGTCTGTCTGTCTGTAGCTGTGTAGTCATTTCCAGGTTTAGTCGCAGGAGT 2740
Qy      68 LeuSerCyseLys-----GlyArgCysepheGluSerPhe 78
Db      2739 CTTAGTTGTAGGTACACCAGGTTCTTGGGACTGTTTCAAGAGCTTT 2692
RESULT 4
af056218/c
; TOIG of: af056218 check: 414 from: 1 to: 1855
; LOCUS AF056218 1855 bp mRNA linear MAM 05-MAR-1999
; DEFINITION Bos taurus superficial zone protein mRNA, partial cds.
; ACCESSION AF056218
; VERSION AF056218.1 GI:3676500
; KEYWORDS
; SOURCE Bos taurus (cow)
; ORGANISM Bos taurus
; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
; Bovinae; Bovinae; Bos.
; REFERENCE 1 (bases 1 to 1855)
; AUTHORS Flannery,C.R., Hughes,C.E., Schumacher,B.L., Tudor,D.,
; Aydelotte,M.B., Kuettnner,K.E. and Caterson,B.
; TITLE Articular cartilage superficial zone protein (SZP) is homologous to
; megakaryocyte stimulating factor precursor and is a multifunctional
; proteoglycan with potential growth-promoting, cytoprotective, and
; lubricating properties in cartilage metabolism
; JOURNAL Biochem. Biophys. Res. Commun. 254 (3), 535-541 (1999)
; MEDLINE 99120896
; PUBMED 9920774
; REFERENCE 2 (bases 1 to 1855)
; AUTHORS Schumacher,B.L., Hughes,C.E., Kuettner,K.E., Caterson,B. and
; Aydelotte,M.B.
; TITLE Immunodetection and partial cDNA sequence of the proteoglycan,
; superficial zone protein, synthesized by cells lining synovial
; joints
```

```
J. Orthop. Res. 17 (1), 110-120 (1999)
99171663
MEDLINE
PUBMED
10073655
REFERENCE
3 (bases 1 to 1855)
AUTHORS
Schumacher,B.L.
TITLE
Direct Submission
JOURNAL
Submitted (31-MAR-1998) Biochemistry Jclke 1306, Rush University,
1653 W. Congress Pkwy., Chicago, IL 60612, USA
FEATURES
Location/Qualifiers
1..1855
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cell_type="chondrocyte"
/tissue_type="articular cartilage"
<1..1206
/codon_start=1
/product="superficial zone protein"
/protein_id="AAD13404.1"
/db_xref="GI:3676501"
/translation="EPPVPKGRATNSQVTPKPKTKAPKPKTKPKPTPRVRKPK
TTPTPKTTTSAMPETPTSLPEMLQTTTRPTPTPNSSEIIVNSSENGDAAEGEK
HMIFRPVITVIPETELIVPGSPGNGENFSDENLNCGRPDVGLITURNGLTV
AFRGHYFWMLTPTPPPPRRITEVWGIESPIDVTRCNCCEGKTFPPKGSQYWRFTN
DIRKAGYPLKISGFGGLNGKIVAAISIAQYKSPESVYFFRGGSVQQYTYKBPQTQ
KCTGRPAINYSVYGTAQVRRRRRPERAIGPSQVHTIRIHYTPVRVPYQDKGFLHNEV
KYSTLWRGLPNVVTSAISLPNIRKPDGYDVALSKDQYVNIIDVPSRTARAITTRSGQT
LSNTWYNCP"
BASE COUNT 638 a 418 c 312 g 487 t
ORIGIN
AF056218 Length: 1855 February 4, 2004 16:21. Type: N Check: 414 ..
af056218
Alignment Scores:
Pred. No.: 0 Length: 1855
Score: 40.50 Matches: 18
Percent Similarity: 37.04% Conservative: 12
Best Local Similarity: 22.22% Mismatches: 30
Query Match: 0.54% Indels: 21
DB: 1 Gaps: 4
US-09-556-246-1 (1-1404) x af056218 (1-1855)
Qy 6 LeuProIleTyrLeuLeuLeuLeuSerValPheValIleGlnGlnValSerSerGln 25
Db 1490 ATTCAGTTTATCTTTTCTTTCTTTATAGGTGAGCCATCGGAGGAGGAG 1431
Qy 26 Asp---LeuSerSerCysAlaGlyArgCysGlyGluGlyTyrSerArgAspAlaThrCys 44
Db 1430 GAATAAATAGAGGAATAATTAATTAATGTTCTGTAACTATATAT----- 1386
Qy 45 AsnCysAspTyrAsnGlnHisTyrMetGluCysCysProAsp----- 59
Db 1385 AACTGTGAATAAGATTGTGAG-----ATCTGTTTGTAGTGAATGACTATCGAG 1338
Qy 60 -----PheIysArgValCysThrAlaGluLeuSerCysIysGlyArg 73
Db 1337 TTTAAACAATTTTGTATTAAAGTTGGTGTCTTCAACGTTCTTTTATTATAAAA 1278
Qy 74 Cys 74
Db 1277 TGT 1275
Search completed: February 4, 2004, 16:36:53
Job time : 34 secs
```